Amendments to the Specification:

Please replace paragraph 3 on page 6 with the following amended paragraphs:

PCR Amplification and DNA sequencing. PCR amplification of the *DRD4* promoter polymorphism was conducted as described (18,19). The program OLIGO 6.0 was used to select primer pairs for the exon 1 polymorphism (20) (5'-TGGGCCGCCGCATTCGT-3' (SEQ.ID.NO. 71) and 5'-GTGGGTGTATCGCCGAGGGA-3' (SEQ.ID.NO. 72); 661-nucleotide product) and the exon 3 VNTR (2) (5'-CGTACTGTGCGGCCTCAACGA-3' (SEQ.ID.NO. 73) and 5'-GACACAGCGCCTGCGTGATGT-3' (SEQ.ID.NO. 74); 705 nucleotide product for the 4R-allele). For some amplifications of the VNTR, primers described previously were used (2). The alternative primers were chosen farther from the VNTR, to minimize out-of-register hybridization during amplification. PCR reactions were conducted in 25 microliter volumes, containing100ng genomic DNA, 200 micromolar dXTPs, 0.5 micromole of each primer, 1X PCR buffer (Qiagen),1X Q-solution (Qiagen) and 0.625 units *Taq* DNA polymerase (Qiagen). Amplification was performed using Perkin-Elmer 9700 thermal cyclers. A 20 second, 96-degrees C hot start was used, followed by 40 cycles of 95 degrees C for 20 seconds and 68 degrees C for 1 minute. Following a 4-minute chase at 72-degrees C, excess primers were eliminated with 0.5 units of Shrimp Alkaline Phosphatase (SAP, Amersham Life Science), 0.1 unit of Exonuclease I (Exo I, Amersham Life Science) and 1X SAP buffer (Amersham Life Science). The SAP/Exo I reaction was carried out at 37 degrees C for 1 hour, followed by a 15-minute heat inactivation at 72-degrees C. The DNA from the SAP/Exo I reaction was used directly for DNA sequencing. For most individuals, the two allelic PCR products were first separated on 1.2-% agarose gels. DNA cycle sequencing was conducted by standard techniques, using ABI 377 and 3700 automated sequencers (21). DNA sequences of the DRD4 haplotypes reported in this paper have been submitted to GenBank (Accession numbers AF395210 through AF395264).